

36063.32 Da. The predicted domains of the BM-HABP polypeptide are: an HA binding motif domain (amino acid residues Q-121 to L-215 of SEQ ID NO:11), double underlined.

Figures 5A-G show the regions of identity between the amino acid sequence of the full-length WF-HABP protein (SEQ ID NO:2) and the translation product of the human TSG-6 protein (SEQ ID NO:3; See Genbank Accession No. gi|339994), as determined by Megalign (DNA Star suite of programs) analysis. Identical amino acids between the two polypeptides are shaded, while the non-identical regions remain unshaded. By examining the regions of amino acids shaded and/or unshaded, the skilled artisan can readily identify conserved domains between the two polypeptides.

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Figures 6A-B show the regions of identity between the amino acid sequence of the WF-HABP protein (SEQ ID NO:5) and the translation product of the human TSG-6 protein (SEQ ID NO:3; See Genbank Accession No. gi|339994), as determined by Megalign (DNA Star suite of programs) analysis. Identical amino acids between the two polypeptides are shaded, while the non-identical regions remain unshaded. By examining the regions of amino acids shaded and/or unshaded, the skilled artisan can readily identify conserved domains between the two polypeptides.

Figure 7 shows the regions of identity between the amino acid sequence of the OE-HABP protein (SEQ ID NO:8) and the translation product of the Cartilage Link Protein from Gallus gallus (SEQ ID NO:9; See Genbank Accession No. gi|212260), as determined by Megalign (DNA Star suite of programs) analysis. Identical amino acids between the two polypeptides are shaded, while the non-identical regions remain unshaded. By examining the regions of amino acids shaded and/or unshaded, the skilled artisan can readily identify conserved domains between the two polypeptides.

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Figure 8 shows the regions of identity between the amino acid sequence of the BM-HABP protein (SEQ ID NO:11) and the translation product of the TSG-6 protein from *Mus musculus* (SEQ ID NO:12; See Genbank Accession No. 2062475), as determined by Megalign (DNA Star suite of programs) analysis. Identical amino acids between the two polypeptides are shaded, while the non-identical regions remain unshaded. By examining the regions of amino acids shaded and/or unshaded, the skilled artisan can readily identify conserved domains between the two polypeptides.

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Please amend the paragraphs from page 15, line 17 to page 16, line 15 as follows:

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The present invention provides isolated nucleic acid molecules comprising polynucleotides encoding a full-length WF-HABP polypeptide (Figures 1A-H (SEQ ID NO:2)). The full-length WF-HABP protein shown in Figures 1A-H (SEQ ID NO:2) shares sequence homology with the human TSG-6 protein (Figures 5A-G (SEQ ID NO:3)).

The present invention provides isolated nucleic acid molecules comprising polynucleotides encoding a WF-HABP polypeptide (Figures 2A-B (SEQ ID NO:5)), the amino acid sequence of which was determined by sequencing a cloned cDNA (Clone HWFBG79). The WF-HABP protein shown in Figures 2A-B (SEQ ID NO:5) shares sequence homology with human cartilage link protein (Figure 6 (SEQ ID NO:6)). The nucleotide sequence shown in Figures 2A-B (SEQ ID NO:4) was obtained by sequencing a cDNA clone (Clone HWFBG79). On December 1, 1998, the plasmid corresponding to this clone was deposited with the American Type Culture Collection, 10801 University Blvd, Manassas, Virginia, 20110-2209, and was assigned accession number 203503. The deposited cDNA is contained in the pBluescript plasmid (Stratagene, La Jolla, CA).

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The present invention provides isolated nucleic acid molecules comprising polynucleotides encoding a OE-HABP polypeptide (Figures 3A-B (SEQ ID NO:8)), the amino acid sequence of which was determined by sequencing a cloned cDNA (Clone HOEDH76). The OE-HABP protein shown in Figures 3A-B (SEQ ID NO:8) shares sequence homology with the Gallus gallus cartilage link protein (Figure 7 (SEQ ID NO:9)). The nucleotide sequence shown in Figures 3A-B (SEQ ID NO:7) was obtained by sequencing a cDNA clone (Clone HOEDH76). On December 1, 1998, the plasmid corresponding to this clone was deposited with the American Type Culture Collection, 10801 University Blvd, Manassas, Virginia, 20110-2209, and was assigned accession number 203501. The deposited cDNA is contained in the pBluescript plasmid (Stratagene, La Jolla, CA).

The present invention provides isolated nucleic acid molecules comprising polynucleotides encoding a BM-HABP polypeptide (Figures 4A-B (SEQ ID NO:11)), the amino acid sequence of which was determined by sequencing a cloned cDNA (Clone HB MVC21). The BM-HABP protein shown in Figures 4A-B (SEQ ID NO:11) shares sequence homology with the Mus musculus TSG-6 protein (Figure 8 (SEQ ID NO:12)). The nucleotide sequence shown in Figures 4A-B (SEQ ID NO:10) was obtained by sequencing a cDNA clone (Clone HB MVC21). On December 1, 1998, the plasmid corresponding to this clone was deposited with the American Type Culture Collection, 10801 University Blvd, Manassas, Virginia, 20110-2209, and was assigned accession number 203502. The deposited cDNA is contained in the pBluescript plasmid (Stratagene, La Jolla, CA).

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Please amend the paragraphs from page 19, line 16 to page 20, line 33 as follows:

The determined nucleotide sequence of the full-length WF-HABP cDNA of

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Figures 1A-H (SEQ ID NO:1) contains an open reading frame encoding a polytopic polypeptide of about 2100 amino acid residues, with a HA-binding domain, EGF-like Type 1 domains, EGF-like Type 2 domains; laminin-type EGF domains; link protein domain; cytochrome P450 cysteine heme-iron ligand binding domains; a prokaryotic membrane lipoprotein lipid attachment site domains, and having a deduced molecular weight of about 231445.37 Da. The WF-HABP protein shown in Figures 1A-H (SEQ ID NO:2) is predicted to contain domains which are about 48% identical to the human hyaluronan binding protein TSG-6 protein depicted in SEQ ID NO:6 (see Figures 5A-G) using the computer program "MegAlign" (DNASTAR suite of software programs). In addition to having homology, TSG-6 and the full-length WF-HABP are thought to share the same topological structure based upon their intrinsic hyaluronan binding activity. For example, like TSG-6, the full-length WF-HABP contains a hyaluronan binding domain. As discussed above, TSG-6 has been shown to be a hyaluronan binding protein and play a vital role in arthritis, antiinflammatory activity, and the vascular injury response.

The determined nucleotide sequence of the WF-HABP cDNA of Figures 2A-B (SEQ ID NO:4) contains an open reading frame encoding a polytopic polypeptide of about 457 amino acid residues, with a HA-binding domain, an EGF-like Type 2 domain, and a link protein domain, and having a deduced molecular weight of about 48448.90 Da. The WF-HABP protein shown in Figures 2A-B (SEQ ID NO:5) is predicted to be about 48% identical to the human hyaluronan binding protein TSG-6 protein depicted in SEQ ID NO:6 (see Figure 6) using the computer program "MegAlign" (DNASTAR suite of software programs). In addition to having homology, TSG-6 and WF-HABP are thought to share

the same topological structure based upon their intrinsic hyaluronan binding activity. For example, like TSG-6, WF-HABP contains a hyaluronan binding domain. As discussed above, TSG-6 has been shown to be a hyaluronan binding protein and play a vital role in arthritis, antiinflammatory activity, and the vascular injury response.

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The determined nucleotide sequence of the OE-HABP cDNA of Figures 3A-B (SEQ ID NO:7) contains an open reading frame encoding a polytopic polypeptide of about 289 amino acid residues, with a HA-binding domain, 6 transmembrane domains, 4 extracellular domains, and a pore loop, and having a deduced molecular weight of about 33174.55 Da. The OE-HABP protein shown in Figures 3A-B (SEQ ID NO:8) is predicted to be about 49% identical to the collagen link protein depicted in SEQ ID NO:9 (see Figure 7) using the computer program "MegAlign" (DNASTAR suite of software programs). In addition to having homology, collagen link protein and OE-HABP are thought to share the same topological structure based upon their intrinsic hyaluronan binding activity. For example, like collagen link protein, OE-HABP contains a hyaluronan binding domain. As discussed above, collagen link protein has been shown to be a hyaluronan binding protein and play a vital role in arthritis, antiinflammatory activity, and the vascular injury response.

The determined nucleotide sequence of the BM-HABP cDNA of Figures 4A-B (SEQ ID NO:10) contains an open reading frame encoding a polytopic polypeptide of about 353 amino acid residues, with a HA-binding domain, 6 transmembrane domains, 4 extracellular domains, and a pore loop, and having a deduced molecular weight of about 36063.32 Da. The BM-HABP protein shown in Figures 4A-B (SEQ ID NO:11) is predicted to be about 43% identical to the TSG-6 protein depicted in SEQ ID NO:12 (see Figure 8) using the computer program "MegAlign" (DNASTAR suite of software programs).

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In addition to having homology, the TSG-6 protein and BM-HABP are thought to share the same topological structure based upon their intrinsic hyaluronan binding activity. For example, like the TSG-6 protein, BM-HABP contains a hyaluronan binding domain. As discussed above, TSG-6 protein has been shown to be a hyaluronan binding protein and play a vital role in arthritis, antiinflammatory activity, and the vascular injury response.

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